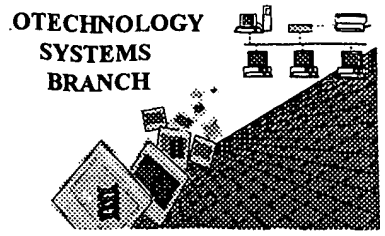

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/077,817C
Source: 1600
Date Processed by STIC: 5/20/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

1600

RAW SEQUENCE LISTING DATE: 05/20/2003
PATENT APPLICATION: **US/09/077,817C** TIME: 13:57:59

Input Set : **A:\SEQID924-09 077817.txt**
Output Set: **N:\CRF4\05202003\I077817C.raw**

```
 3 <110> APPLICANT: Caput, Daniel
 4       Ferrara, Pascual
 5       Laurent, Patrick
 6       Vita, Natalio
 8 <120> TITLE OF INVENTION: IL-13 RECEPTOR
10 <130> FILE REFERENCE: IVD924
12 <140> CURRENT APPLICATION NUMBER: 09/077,817C
13 <141> CURRENT FILING DATE: 1998-09-14
15 <150> PRIOR APPLICATION NUMBER: PCT/FR96/01756
16 <151> PRIOR FILING DATE: 1996-11-07
18 <160> NUMBER OF SEQ ID NOS: 15
20 <170> SOFTWARE: PatentIn Ver. 2.0
```

FYI: all bases MUST be in lower-case letters, when Sequence Listing is in "new" Sequence Rules format (Please correct ALL nucleotide sequences)

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1539
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
```

1298 shown

```
C--> 29 ggtgcctgtc ggcggggaga gaggcaatat caaggtttta aatctcggag aaatggcttt     60
     31 cgtttgcttg gctatcggat gcttatatac ctttctgata agcacaacat ttggctgtac    120
     33 ttcatcttca gacaccgaga taaaagttaa ccctcctcag gattttgaga tagtggatcc    180
     35 cggatactta ggttatctct atttgcaatg gcaaccccca ctgtctctgg atcattttaa    240
     37 ggaatgcaca gtggaatatg aactaaaata ccgaaacatt ggtagtgaaa catggaagac    300
     39 catcattact aagaatctac attacaaaga tgggtttgat cttaacaagg gcattgaagc    360
     41 gaagatacac acgcttttac catggcaatg cacaaatgga tcagaagttc aaagttcctg    420
     43 ggcagaaact acttattgga tatcaccaca aggaattcca gaaactaaag ttcaggatat    480
     45 ggattgcgta tattacaatt ggcaatattt actctgttct tggaaacctg gcataggtgt    540
     47 acttcttgat accaattaca acttgtttta ctggtatgag ggcttggatc atgcattaca    600
     49 gtgtgttgat tacatcaagg ctgatggaca aaatatagga tgcagatttc cctatttgga    660
     51 ggcatcagac tataaagatt tctatatttg tgttaatgga tcatcagaga acaagcctat    720
     53 cagatccagt tatttcactt ttcagcttca aaatatagtt aaacctttgc cgccagtcta    780
     55 tcttactttt actcgggaga gttcatgtga aattaagctg aaatggagca tacctttggg    840
     57 acctattcca gcaaggtgtt ttgattatga aattgagatc agagaagatg atactacctt    900
     59 ggtgactgct acagttgaaa atgaaacata caccttgaaa acaacaaatg aaacccgaca    960
     61 attatgcttt gtagtaagaa gcaaagtgaa tatttattgc tcagatgacg gaatttggag   1020
     63 tgagtggagt gataaacaat gctgggaagg tgaagaccta tcgaagaaaa ctttgctacg   1080
     65 tttctggcta ccatttggtt tcatcttaat attagttata tttgtaaccg gtctgctttt   1140
     67 gcgtaagcca aacacctacc caaaaatgat tccagaattt ttctgtgata catgaagact   1200
     69 ttccatatca agagacatgg tattgactca acagtttcca gtcatggcca aatgttcaat   1260
E--> 71 atgagtctca ataaactgaa tttttcttgc gaatgttg                         1298
```

RAW SEQUENCE LISTING DATE: 05/20/2003
PATENT APPLICATION: US/09/077,817C TIME: 13:57:59

Input Set : A:\SEQID924-09 077817.txt
Output Set: N:\CRF4\05202003\I077817C.raw

```
     339 <210> SEQ ID NO: 5
     340 <211> LENGTH: 420
     341 <212> TYPE: PRT
     342 <213> ORGANISM: Homo sapiens
     344 <400> SEQUENCE: 5
     346 Met Ile Ile Val Ala His Val Leu Leu Ile Leu Leu Gly Ala Thr Glu
E--> 347
  1               5                  10                  15
E--> 348            20                  25                  30
     349 Pro Val Asn Phe Thr Ile Lys Val Thr Gly Leu Ala Gln Val Leu Leu
E--> 350          35                  40                  45
     351 Gln Trp Lys Pro Asn Pro Asp Gln Glu Gln Arg Asn Val Asn Leu Glu
E--> 352      50                  55                  60
     353 Tyr Gln Val Lys Ile Asn Ala Pro Lys Glu Asp Asp Tyr Glu Thr Arg
E--> 354  65                  70                  75                  80
     355 Ile Thr Glu Ser Lys Cys Val Thr Ile Leu His Lys Gly Phe Ser Ala
E--> 356                  85                  90                  95
     357 Ser Val Arg Thr Ile Leu Gln Asn Asp His Ser Leu Leu Ala Ser Ser
E--> 358              100                 105                 110
     359 Trp Ala Ser Ala Glu Leu His Ala Pro Pro Gly Ser Pro Gly Thr Ser
E--> 360          115                 120                 125
     361 Ile Val Asn Leu Thr Cys Thr Thr Asn Thr Thr Glu Asp Asn Tyr Ser
E--> 362      130                 135                 140
     363 Arg Leu Arg Ser Tyr Gln Val Ser Leu His Cys Thr Trp Leu Val Gly
E--> 364 145                 150                 155                 160
     365 Thr Asp Ala Pro Glu Asp Thr Gln Tyr Phe Leu Tyr Tyr Arg Tyr Gly
E--> 366                  165                 170                 175
     367 Ser Trp Thr Glu Glu Cys Gln Glu Tyr Ser Lys Asp Thr Leu Gly Arg
E--> 368              180                 185                 190
     369 Asn Ile Ala Cys Trp Phe Pro Arg Thr Phe Ile Leu Ser Lys Gly Arg
E--> 370          195                 200                 205
     371 Asp Trp Leu Ser Val Leu Val Asn Gly Ser Ser Lys His Ser Ala Ile
E--> 372      210                 215                 220
     373 Arg Pro Phe Asp Gln Leu Phe Ala Leu His Ala Ile Asp Gln Ile Asn
E--> 374 225                 230                 235                 240
     375 Pro Pro Leu Asn Val Thr Ala Glu Ile Glu Gly Thr Arg Leu Ser Ile
E--> 376                  245                 250                 255
     377 Gln Trp Glu Lys Pro Val Ser Ala Phe Pro Ile His Cys Phe Asp Tyr
E--> 378              260                 265                 270
     379 Glu Val Lys Ile His Asn Thr Arg Asn Gly Tyr Leu Gln Ile Glu Lys
E--> 380          275                 280                 285
     381 Leu Met Thr Asn Ala Phe Ile Ser Ile Ile Asp Asp Leu Ser Lys Tyr
E--> 382      290                 295                 300
     383 Asp Val Gln Val Arg Ala Ala Val Ser Ser Met Cys Arg Glu Ala Gly
E--> 384 305                 310                 315                 320
     385 Leu Trp Ser Glu Trp Ser Gln Pro Ile Tyr Val Gly Asn Asp Glu His
E--> 386                  325                 330                 335
     387 Lys Pro Leu Arg Glu Trp Phe Val Ile Val Ile Met Ala Thr Ile Cys
E--> 388              340                 345                 350
     390 Phe Ile Leu Leu Ile Leu Ser Leu Ile Cys Lys Ile Cys His Leu Trp
```

?

Please ensure TAB codes are NOT used. They cause format errors.

see next page

RAW SEQUENCE LISTING DATE: 05/20/2003
PATENT APPLICATION: US/09/077,817C TIME: 13:57:59

Input Set : A:\SEQID924-09 077817.txt
Output Set: N:\CRF4\05202003\I077817C.raw

```
E--> 391          355                 360                 365
     392 Ile Lys Leu Phe Pro Pro Ile Pro Ala Pro Lys Ser Asn Ile Lys Asp
E--> 393      370                 375                 380
     394 Leu Phe Val Thr Thr Asn Tyr Glu Lys Ala Gly Ser Ser Glu Thr Glu
E--> 395 385                 390                 395                 400
     396 Ile Glu Val Ile Cys Tyr Ile Glu Lys Pro Gly Val Glu Thr Leu Glu
E--> 397                 405                 410                 415
E--> 398
Asp Ser Val Phe                                                      42C
     402 <210> SEQ ID NO: 6
     403 <211> LENGTH: 424
     404 <212> TYPE: PRT
     405 <213> ORGANISM: Mus musculus
     407 <400> SEQUENCE: 6
     409 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
     410   1               5                  10                  15
     412 Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro
     413              20                  25                  30
     415 Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp
     416          35                  40                  45
     418 Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
     419      50                  55                  60
     421 Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr
     422  65                  70                  75                  80
     424 His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val
     425                  85                  90                  95
     427 Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val
     428             100                 105                 110
     430 Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Arg Glu Ser Ala Val Thr
     431         115                 120                 125
     433 Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp
     434     130                 135                 140
     436 Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr
     437 145                 150                 155                 160
     439 Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg
     440                 165                 170                 175
     442 Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro
     443             180                 185                 190
     445 Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly
     446         195                 200                 205
     448 Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys
     449     210                 215                 220
     451 Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu
     452 225                 230                 235                 240
     454 Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr
     455                 245                 250                 255
     457 Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu
     458             260                 265                 270
     460 Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met
     461         275                 280                 285
```

p.4

RAW SEQUENCE LISTING DATE: 05/20/2003
PATENT APPLICATION: US/09/077,817C TIME: 13:57:59

Input Set : A:\SEQID924-09 077817.txt
Output Set: N:\CRF4\05202003\I077817C.raw

```
463 Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val
464     290                 295                 300
466 Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp
467 305                 310                 315                 320
469 Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu
470                 325                 330                 335
472 Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe
473             340                 345                 350
475 Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys
476         355                 360                 365
478 Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu
479     370                 375                 380
481 Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp
482 385                 390                 395                 400
484 Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile
485                 405                 410                 415
486
                                                    Glu Asn Leu Lys
E--> 487             420
```

644 <210> SEQ ID NO: 15
645 <211> LENGTH: 20
646 <212> TYPE: DNA
647 <213> ORGANISM: Artificial sequence
649 <220> FEATURE:
650 <223> OTHER INFORMATION: primer
653 <400> SEQUENCE: 15
C--> 655 aaaaaaaaaa aaagggcccg 20
E--> 657 1
E--> 660 37 delete

see following pages for more errors

<210> 11
<211> 6
<212> PRT
<213> Artificial sequence

? This sequence is Sequence 11

<220>
<223> in SEQ ID NO. 12 which is a variant of SEQ ID NO. 2, the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

<400> 11
Val Arg Cys Val Thr Leu
1 5

<210> 13
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> motif characteristic of the family of chemokine receptors to which the polypeptides of SEQ ID NO. 2 and SEQ NO. 4 belong. Xaa can be any amino acid.

<400> 13

Trp Ser Xaa Trp Ser
1 5

Per 1.823 of Sequence Rules, use this format for Xaa's or n's:

<2227 (1)...(5) ← first amino acid and last amino acid positions (that way, all positions are covered)
<2237 Xaa can be any amino acid.

VERIFICATION SUMMARY DATE: 05/20/2003
PATENT APPLICATION: **US/09/077,817C** TIME: 13:58:00

Input Set : **A:\SEQID924-09 077817.txt**
Output Set: **N:\CRF4\05202003\I077817C.raw**

L:29 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:71 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1539 Found:1298 SEQ:1
L:139 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=3
L:347 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:5
L:347 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:347 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=5
L:398 M:252 E: No. of Seq. differs, <211> LENGTH:Input:420 Found:408 SEQ:5
L:487 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:500 M:112 C: (48) String data converted to lower case,
L:514 M:112 C: (48) String data converted to lower case,
L:527 M:112 C: (48) String data converted to lower case,
L:539 M:112 C: (48) String data converted to lower case,
L:628 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13
L:628 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
L:628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:642 M:112 C: (48) String data converted to lower case,
L:655 M:112 C: (48) String data converted to lower case,
L:657 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=15

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/20/2003
PATENT APPLICATION: **US/09/077,817C** TIME: 13:58:00

Input Set : **A:\SEQID924-09 077817.txt**
Output Set: **N:\CRF4\05202003\I077817C.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,2,3,4,5,6,7,8,9,11,12,13,14,15,16,17,18,19,20,21,22,23,24
Seq#:1; Line(s) 25,26,75
Seq#:2; Line(s) 76,77,78,79,132
Seq#:3; Line(s) 133,134,135,136,275
Seq#:4; Line(s) 276,277,278,279,339
Seq#:5; Line(s) 340,341,343,346,347,348,349,350,351,352,353,354,355,356,357
Seq#:5; Line(s) 358,359,360,361,362,363,364,365,366,367,368,369,370,371,372
Seq#:5; Line(s) 373,374,375,376,377,378,379,380,381,382,383,384,385,386,387
Seq#:5; Line(s) 388,389,390,391,392,393,394,395,396,397,398,402
Seq#:6; Line(s) 403,404,405,406,409,410,411,412,413,414,415,416,417,418,419
Seq#:6; Line(s) 420,421,422,423,424,425,426,427,428,429,430,431,432,433,434
Seq#:6; Line(s) 435,436,437,438,439,440,441,442,443,444,445,446,447,448,449
Seq#:6; Line(s) 450,451,452,453,454,455,456,457,458,459,460,461,462,463,464
Seq#:6; Line(s) 465,466,467,468,469,470,471,472,473,474,475,476,477,478,479
Seq#:6; Line(s) 480,481,482,483,484,485,486,487,490
Seq#:7; Line(s) 492,497,503
Seq#:8; Line(s) 505,511,517
Seq#:9; Line(s) 519,524,529
Seq#:10; Line(s) 531,536,542
Seq#:11; Line(s) 544,548,549,556
Seq#:12; Line(s) 557,558,562,563,618
Seq#:13; Line(s) 620,624,632
Seq#:14; Line(s) 634,644
Seq#:15; Line(s) 646,652

VARIABLE LOCATION SUMMARY DATE: 05/20/2003
PATENT APPLICATION: US/09/077,817C TIME: 13:58:00

Input Set : A:\SEQID924-09 077817.txt
Output Set: N:\CRF4\05202003\I077817C.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:13; Xaa Pos. 3